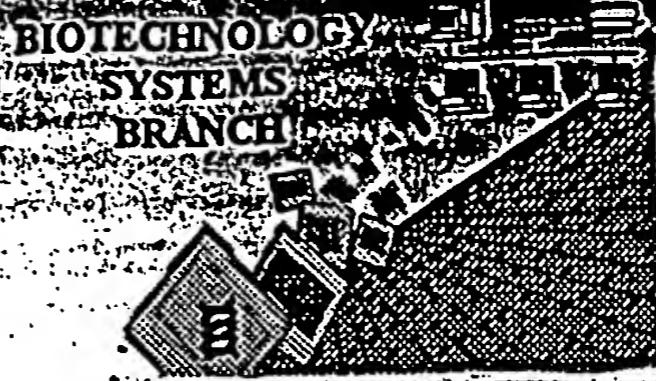


**RAW SEQUENCE LISTING
ERROR REPORT**



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Source: OIRPE
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FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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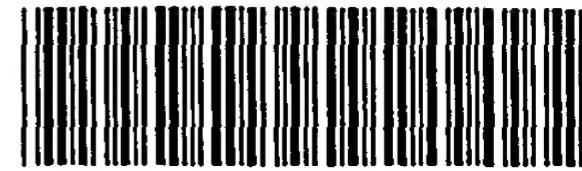
1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>>), EFS Submission User Manual - ePAVE)
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Output Set: N:\CRF3\05312002\J014099A.raw

AUG 15 2002

5 <110> APPLICANT: KUEHN, Ralf
6 FELDER, Susanne
7 SCHWENK, Frieder
8 KUETER LUKS, Birgit
9 FAUST, Nicole
11 <120> TITLE OF INVENTION: Modified Recombinase
13 <130> FILE REFERENCE: 012787wo/JH/ml
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/014,099A
C--> 16 <141> CURRENT FILING DATE: 2001-12-11
18 <160> NUMBER OF SEQ ID NOS: 108
20 <170> SOFTWARE: PatentIn Ver. 2.1

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changed to
PRT

1408 <210> SEQ ID NO: 23
1409 <211> LENGTH: 620
1410 <212> TYPE: DNA
1411 <213> ORGANISM: Artificial Sequence
W--> 1412 <220> FEATURE:
1413 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
1414 encoding the fusion protein C31-Int(CNLS)
1416 <400> SEQUENCE: 23
1417 Met Thr Gln Gly Val Val Thr Gly Val Asp Thr Tyr Ala Gly Ala Tyr
1418 1 5 10 15
1420 Asp Arg Gln Ser Arg Glu Arg Glu Asn Ser Ser Ala Ala Ser Pro Ala
1421 20 25 30
1423 Thr Gln Arg Ser Ala Asn Glu Asp Lys Ala Ala Asp Leu Gln Arg Glu
1424 35 40 45
1426 Val Glu Arg Asp Gly Gly Arg Phe Arg Phe Val Gly His Phe Ser Glu
1427 50 55 60
1429 Ala Pro Gly Thr Ser Ala Phe Gly Thr Ala Glu Arg Pro Glu Phe Glu
1430 65 70 75 80
1432 Arg Ile Leu Asn Glu Cys Arg Ala Gly Arg Leu Asn Met Ile Ile Val
1433 85 90 95
1435 Tyr Asp Val Ser Arg Phe Ser Arg Leu Lys Val Met Asp Ala Ile Pro
1436 100 105 110
1438 Ile Val Ser Glu Leu Leu Ala Leu Gly Val Thr Ile Val Ser Thr Gln
1439 115 120 125
1441 Glu Gly Val Phe Arg Gln Gly Asn Val Met Asp Leu Ile His Leu Ile
1442 130 135 140
1444 Met Arg Leu Asp Ala Ser His Lys Glu Ser Ser Leu Lys Ser Ala Lys
1445 145 150 155 160

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DATE: 05/31/2002
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Output Set: N:\CRF3\05312002\J014099A.raw

1447 Ile Leu Asp Thr Lys Asn Leu Gln Arg Glu Leu Gly Gly Tyr Val Gly
1448 165 170 175
1450 Gly Lys Ala Pro Tyr Gly Phe Glu Leu Val Ser Glu Thr Lys Glu Ile
1451 180 185 190
1453 Thr Arg Asn Gly Arg Met Val Asn Val Val Ile Asn Lys Leu Ala His
1454 195 200 205
1456 Ser Thr Thr Pro Leu Thr Gly Pro Phe Glu Phe Glu Pro Asp Val Ile
1457 210 215 220
1459 Arg Trp Trp Trp Arg Glu Ile Lys Thr His Lys His Leu Pro Phe Lys
1460 225 230 235 240
1462 Pro Gly Ser Gln Ala Ala Ile His Pro Gly Ser Ile Thr Gly Leu Cys
1463 245 250 255
1465 Lys Arg Met Asp Ala Asp Ala Val Pro Thr Arg Gly Glu Thr Ile Gly
1466 260 265 270
1468 Lys Lys Thr Ala Ser Ser Ala Trp Asp Pro Ala Thr Val Met Arg Ile
1469 275 280 285
1471 Leu Arg Asp Pro Arg Ile Ala Gly Phe Ala Ala Glu Val Ile Tyr Lys
1472 290 295 300
1474 Lys Lys Pro Asp Gly Thr Pro Thr Thr Lys Ile Glu Gly Tyr Arg Ile
1475 305 310 315 320
1477 Gln Arg Asp Pro Ile Thr Leu Arg Pro Val Glu Leu Asp Cys Gly Pro
1478 325 330 335
1480 Ile Ile Glu Pro Ala Glu Trp Tyr Glu Leu Gln Ala Trp Leu Asp Gly
1481 340 345 350
1483 Arg Gly Arg Gly Lys Gly Leu Ser Arg Gly Gln Ala Ile Leu Ser Ala
1484 355 360 365
1486 Met Asp Lys Leu Tyr Cys Glu Cys Gly Ala Val Met Thr Ser Lys Arg
1487 370 375 380
1489 Gly Glu Glu Ser Ile Lys Asp Ser Tyr Arg Cys Arg Arg Arg Lys Val
1490 385 390 395 400
1492 Val Asp Pro Ser Ala Pro Gly Gln His Glu Gly Thr Cys Asn Val Ser
1493 405 410 415
1495 Met Ala Ala Leu Asp Lys Phe Val Ala Glu Arg Ile Phe Asn Lys Ile
1496 420 425 430
1498 Arg His Ala Glu Gly Asp Glu Glu Thr Leu Ala Leu Leu Trp Glu Ala
1499 435 440 445
1501 Ala Arg Arg Phe Gly Lys Leu Thr Glu Ala Pro Glu Lys Ser Gly Glu
1502 450 455 460
1504 Arg Ala Asn Leu Val Ala Glu Arg Ala Asp Ala Leu Asn Ala Leu Glu
1505 465 470 475 480
1507 Glu Leu Tyr Glu Asp Arg Ala Ala Gly Ala Tyr Asp Gly Pro Val Gly
1508 485 490 495
1510 Arg Lys His Phe Arg Lys Gln Gln Ala Ala Leu Thr Leu Arg Gln Gln
1511 500 505 510
1513 Gly Ala Glu Glu Arg Leu Ala Glu Leu Glu Ala Ala Glu Ala Pro Lys
1514 515 520 525
1516 Leu Pro Leu Asp Gln Trp Phe Pro Glu Asp Ala Asp Ala Asp Pro Thr
1517 530 535 540
1519 Gly Pro Lys Ser Trp Trp Gly Arg Ala Ser Val Asp Asp Lys Arg Val

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Input Set : A:\PTOMS.txt
Output Set: N:\CRF3\05312002\J014099A.raw

1520 545 550 555 560
1522 Phe Val Gly Leu Phe Val Asp Lys Ile Val Val Thr Lys Ser Thr Thr
1523 565 570 575
1525 Gly Arg Gly Gln Gly Thr Pro Ile Glu Lys Arg Ala Ser Ile Thr Trp
1526 580 585 590
1528 Ala Lys Pro Pro Thr Asp Asp Asp Glu Asp Asp Ala Gln Asp Gly Thr
1529 595 600 605
1531 Glu Asp Val Ala Ala Pro Lys Lys Arg Lys Val
E--> 1532 610 615 620
3321 <210> SEQ ID NO: 65
3322 <211> LENGTH: 335
3323 <212> TYPE: PRT
3324 <213> ORGANISM: Artificial Sequence
N--> 3325 <220> FEATURE *<220> is mandatory and needs to be inserted*
3325 <223> OTHER INFORMATION: Description of Artificial Sequence: vector
3326 pBS-SSV3
E--> 3328 <400> SEQUENCE: 65
3329 Met Thr Lys Asp Lys Thr Arg Tyr Lys Tyr Gly Asp Tyr Ile Leu Arg
3330 1 5 10 15
3332 Glu Arg Lys Gly Arg Tyr Tyr Val Tyr Lys Leu Glu Tyr Glu Asn Gly
3333 20 25 30
3335 Glu Val Lys Glu Arg Tyr Val Gly Pro Leu Ala Asp Val Val Glu Ser
3336 35 40 45
3338 Tyr Leu Lys Met Lys Leu Gly Val Val Gly Asp Thr Pro Leu Gln Ala
3339 50 55 60
3341 Asp Pro Pro Gly Phe Glu Pro Gly Thr Ser Gly Ser Gly Gly Lys
3342 65 70 75 80
3344 Glu Gly Thr Glu Arg Arg Lys Ile Ala Leu Val Ala Asn Leu Arg Gln
3345 85 90 95
3347 Tyr Ala Thr Asp Gly Asn Ile Lys Ala Phe Tyr Asn Tyr Leu Met Asn
3348 100 105 110
3350 Glu Arg Gly Ile Ser Glu Lys Thr Ala Lys Asp Tyr Ile Asn Ala Ile
3351 115 120 125
3353 Ser Lys Pro Tyr Lys Glu Thr Arg Asp Ala Gln Lys Ala Tyr Arg Leu
3354 130 135 140
3356 Phe Ala Arg Phe Leu Ala Ser Arg Asn Ile Ile His Asp Glu Phe Ala
3357 145 150 155 160
3359 Asp Lys Ile Leu Lys Ala Val Lys Val Lys Lys Ala Asn Ala Asp Ile
3360 165 170 175
3362 Tyr Ile Pro Thr Leu Glu Glu Ile Lys Arg Thr Leu Gln Leu Ala Lys
3363 180 185 190
3365 Asp Tyr Ser Glu Asn Val Tyr Phe Ile Tyr Arg Ile Ala Leu Glu Ser
3366 195 200 205
3368 Gly Val Arg Leu Ser Glu Ile Leu Lys Val Leu Lys Glu Pro Glu Arg
3369 210 215 220
3371 Asp Ile Cys Gly Asn Asp Val Cys Tyr Tyr Pro Leu Ser Trp Thr Arg
3372 225 230 235 240
3374 Gly Tyr Lys Gly Val Phe Tyr Val Phe His Ile Thr Pro Leu Lys Arg
3375 245 250 255

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Input Set : A:\PTOMS.txt
Output Set: N:\CRF3\05312002\J014099A.raw

3377 Val Glu Val Thr Lys Trp Ala Ile Ala Asp Phe Glu Arg Arg His Lys
3378 260 265 270
3380 Asp Ala Ile Ala Ile Lys Tyr Phe Arg Lys Phe Val Ala Ser Lys Met
3381 275 280 285
3383 Ala Glu Leu Ser Val Pro Leu Asp Ile Ile Asp Phe Ile Gln Gly Arg
3384 290 295 300
3386 Lys Pro Thr Arg Val Leu Thr Gln His Tyr Val Ser Leu Phe Gly Ile
3387 305 310 315 320
3389 Ala Lys Glu Gln Tyr Lys Tyr Ala Glu Trp Leu Lys Gly Val
3390 325 330 335
3529 <210> SEQ ID NO: 67
3530 <211> LENGTH: 479
3531 <212> TYPE: PRT
3532 <213> ORGANISM: Artificial Sequence *<220> is mandatory and needs to be inserted.*
v--> 3533 <220> FEATURE:
3533 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
3534 coding for fusion protein NLS-XisA
v--> 3536 <400> SEQUENCE: 67
3537 Met Pro Lys Lys Lys Arg Lys Val Gln Asn Gln Gly Gln Asp Lys Tyr
3538 1 5 10 15
3540 Gln Gln Ala Phe Ala Asp Leu Glu Pro Leu Ser Ser Thr Asp Gly Ser
3541 20 25 30
3543 Phe Leu Gly Ser Ser Leu Gln Ala Gln Gln Arg Glu His Met Arg
3544 35 40 45
3546 Thr Lys Val Leu Gln Asp Leu Asp Lys Val Asn Leu Arg Leu Lys Ser
3547 50 55 60
3549 Ala Lys Thr Lys Val Ser Val Arg Glu Ser Asn Gly Ser Leu Gln Leu
3550 65 70 75 80
3552 Arg Ala Thr Leu Pro Ile Lys Pro Gly Asp Lys Asp Thr Asn Gly Thr
3553 85 90 95
3555 Gly Arg Lys Gln Tyr Asn Leu Ser Leu Asn Ile Pro Ala Asn Leu Asp
3556 100 105 110
3558 Gly Leu Lys Thr Ala Glu Glu Ala Tyr Glu Leu Gly Lys Leu Ile
3559 115 120 125
3561 Ala Arg Lys Thr Phe Glu Trp Asn Asp Lys Tyr Leu Gly Lys Glu Ala
3562 130 135 140
3564 Thr Lys Lys Asp Ser Gln Thr Ile Gly Asp Leu Leu Glu Lys Phe Ala
3565 145 150 155 160
3567 Glu Glu Tyr Phe Lys Thr His Lys Arg Thr Thr Lys Ser Glu His Thr
3568 165 170 175
3570 Phe Phe Tyr Tyr Phe Ser Arg Thr Gln Arg Tyr Thr Asn Ser Lys Asp
3571 180 185 190
3573 Leu Ala Thr Ala Glu Asn Leu Ile Asn Ser Ile Glu Gln Ile Asp Lys
3574 195 200 205
3576 Glu Trp Ala Arg Tyr Asn Ala Ala Arg Ala Ile Ser Ala Phe Cys Ile
3577 210 215 220
3579 Thr Phe Asn Ile Glu Ile Asp Leu Ser Gln Tyr Ser Lys Met Pro Asp
3580 225 230 235 240
3582 Arg Asn Ser Arg Asn Ile Pro Thr Asp Ala Glu Ile Leu Ser Gly Ile

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Input Set : A:\PTOMS.txt
Output Set: N:\CRF3\05312002\J014099A.raw

3583 245 250 255
3585 Thr Lys Phe Glu Asp Tyr Leu Val Thr Arg Gly Asn Gln Val Asn Glu
3586 260 265 270
3588 Asp Val Lys Asp Ser Trp Gln Leu Trp Arg Trp Thr Tyr Gly Met Leu
3589 275 280 285
3591 Ala Val Phe Gly Leu Arg Pro Arg Glu Ile Phe Ile Asn Pro Asn Ile
3592 290 295 300
3594 Asp Trp Trp Leu Ser Lys Glu Asn Ile Asp Leu Thr Trp Lys Val Asp
3595 305 310 315 320
3597 Lys Glu Cys Lys Thr Gly Glu Arg Gln Ala Leu Pro Leu His Lys Glu
3598 325 330 335
3600 Trp Ile Asp Glu Phe Asp Leu Arg Asn Pro Lys Tyr Leu Glu Met Leu
3601 340 345 350
3603 Ala Thr Ala Ile Ser Lys Lys Asp Lys Thr Asn His Ala Glu Ile Thr
3604 355 360 365
3606 Ala Leu Thr Gln Arg Ile Ser Trp Trp Phe Arg Lys Val Glu Leu Asp
3607 370 375 380
3609 Phe Lys Pro Tyr Asp Leu Arg His Ala Trp Ala Ile Arg Ala His Ile
3610 385 390 395 400
3612 Leu Gly Ile Pro Ile Lys Ala Ala Ala Asp Asn Leu Gly His Ser Met
3613 405 410 415
3615 Gln Val His Thr Gln Thr Tyr Gln Arg Trp Phe Ser Leu Asp Met Arg
3616 420 425 430
3618 Lys Leu Ala Ile Asn Gln Ala Leu Thr Lys Arg Asn Glu Phe Glu Val
3619 435 440 445
3621 Ile Arg Glu Glu Asn Ala Lys Leu Gln Ile Glu Asn Glu Arg Leu Arg
3622 450 455 460
3624 Met Glu Ile Glu Lys Leu Lys Met Glu Ile Ala Tyr Lys Asn Ser
3625 465 470 475

3732 <210> SEQ ID NO: 69

3733 <211> LENGTH: 342

3734 <212> TYPE: PRT

3735 <213> ORGANISM: Artificial Sequence

<210> is mandatory and
needs to be inserted

W--> 3736 <220> FEATURE:

3736 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA sequence

3737 coding for fusion protein NLS-Ssv

E--> 3739 <400> SEQUENCE: 69

3740 Met Pro Lys Lys Lys Arg Lys Val Thr Lys Asp Lys Thr Arg Tyr Lys
3741 1 5 10 15
3743 Tyr Gly Asp Tyr Ile Leu Arg Glu Arg Lys Gly Arg Tyr Tyr Val Tyr
3744 20 25 30
3746 Lys Leu Glu Tyr Glu Asn Gly Glu Val Lys Glu Arg Tyr Val Gly Pro
3747 35 40 45
3749 Leu Ala Asp Val Val Glu Ser Tyr Leu Lys Met Lys Leu Gly Val Val
3750 50 55 60
3752 Gly Asp Thr Pro Leu Gln Ala Asp Pro Pro Gly Phe Glu Pro Gly Thr
3753 65 70 75 80
3755 Ser Gly Ser Gly Gly Lys Glu Gly Thr Glu Arg Arg Lys Ile Ala
3756 85 90 95

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Input Set : A:\PTOMS.txt
Output Set: N:\CRF3\05312002\J014099A.raw

3758 Leu Val Ala Asn Leu Arg Gln Tyr Ala Thr Asp Gly Asn Ile Lys Ala
3759 100 105 110
3761 Phe Tyr Asn Tyr Leu Met Asn Glu Arg Gly Ile Ser Glu Lys Thr Ala
3762 115 120 125
3764 Lys Asp Tyr Ile Asn Ala Ile Ser Lys Pro Tyr Lys Glu Thr Arg Asp
3765 130 135 140
3767 Ala Gln Lys Ala Tyr Arg Leu Phe Ala Arg Phe Leu Ala Ser Arg Asn
3768 145 150 155 160
3770 Ile Ile His Asp Glu Phe Ala Asp Lys Ile Leu Lys Ala Val Lys Val
3771 165 170 175
3773 Lys Lys Ala Asn Ala Asp Ile Tyr Ile Pro Thr Leu Glu Glu Ile Lys
3774 180 185 190
3776 Arg Thr Leu Gln Leu Ala Lys Asp Tyr Ser Glu Asn Val Tyr Phe Ile
3777 195 200 205
3779 Tyr Arg Ile Ala Leu Glu Ser Gly Val Arg Leu Ser Glu Ile Leu Lys
3780 210 215 220
3782 Val Leu Lys Glu Pro Glu Arg Asp Ile Cys Gly Asn Asp Val Cys Tyr
3783 225 230 235 240
3785 Tyr Pro Leu Ser Trp Thr Arg Gly Tyr Lys Gly Val Phe Tyr Val Phe
3786 245 250 255
3788 His Ile Thr Pro Leu Lys Arg Val Glu Val Thr Lys Trp Ala Ile Ala
3789 260 265 270
3791 Asp Phe Glu Arg Arg His Lys Asp Ala Ile Ala Ile Lys Tyr Phe Arg
3792 275 280 285
3794 Lys Phe Val Ala Ser Lys Met Ala Glu Leu Ser Val Pro Leu Asp Ile
3795 290 295 300
3797 Ile Asp Phe Ile Gln Gly Arg Lys Pro Thr Arg Val Leu Thr Gln His
3798 305 310 315 320
3800 Tyr Val Ser Leu Phe Gly Ile Ala Lys Glu Gln Tyr Lys Lys Tyr Ala
3801 325 330 335
3803 Glu Trp Leu Lys Gly Val
3804 340
6191 <210> SEQ ID NO: 108
6192 <211> LENGTH: 485
6193 <212> TYPE: PRT
6194 <213> ORGANISM: Bacteriophage TP901-1
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6200 Ala Glu Glu Gly Phe Ser Ile Asp Glu Gln Ile Asp Arg Leu Thr Lys
6201 20 25 30
6203 Tyr Ala Glu Ala Met Gly Trp Gln Val Ser Asp Thr Tyr Thr Asp Ala
6204 35 40 45
6206 Gly Phe Ser Gly Ala Lys Leu Glu Arg Pro Ala Met Gln Arg Leu Ile
6207 50 55 60
6209 Asn Asp Ile Glu Asn Lys Ala Phe Asp Thr Val Leu Val Tyr Lys Leu
6210 65 70 75 80
6212 Asp Arg Leu Ser Arg Ser Val Arg Asp Thr Leu Tyr Leu Val Lys Asp
6213 85 90 95

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6218 Asp Thr Ser Ser Ala Met Gly Ser Leu Phe Leu Thr Ile Leu Ser Ala
6219 115 120 125
6221 Ile Asn Glu Phe Glu Arg Glu Asn Ile Lys Glu Arg Met Thr Met Gly
6222 130 135 140
6224 Lys Leu Gly Arg Ala Lys Ser Gly Lys Ser Met Met Trp Thr Lys Thr
6225 145 150 155 160
6227 Ala Phe Gly Tyr Tyr His Asn Arg Lys Thr Gly Ile Leu Glu Ile Val
6228 165 170 175
6230 Pro Leu Gln Ala Thr Ile Val Glu Gln Ile Phe Thr Asp Tyr Leu Ser
6231 180 185 190
6233 Gly Ile Ser Leu Thr Lys Leu Arg Asp Lys Leu Asn Glu Ser Gly His
6234 195 200 205
6236 Ile Gly Lys Asp Ile Pro Trp Ser Tyr Arg Thr Leu Arg Gln Thr Leu
6237 210 215 220
6239 Asp Asn Pro Val Tyr Cys Gly Tyr Ile Lys Phe Lys Asp Ser Leu Phe
6240 225 230 235 240
6242 Glu Gly Met His Lys Pro Ile Ile Pro Tyr Glu Thr Tyr Leu Lys Val
6243 245 250 255
6245 Gln Lys Glu Leu Glu Glu Arg Gln Gln Gln Thr Tyr Glu Arg Asn Asn
6246 260 265 270
6248 Asn Pro Arg Pro Phe Gln Ala Lys Tyr Met Leu Ser Gly Met Ala Arg
6249 275 280 285
6251 Cys Gly Tyr Cys Gly Ala Pro Leu Lys Ile Val Leu Gly His Lys Arg
6252 290 295 300
6254 Lys Asp Gly Ser Arg Thr Met Lys Tyr His Cys Ala Asn Arg Phe Pro
6255 305 310 315 320
6257 Arg Lys Thr Lys Gly Ile Thr Val Tyr Asn Asp Asn Lys Lys Cys Asp
6258 325 330 335
6260 Ser Gly Thr Tyr Asp Leu Ser Asn Leu Glu Asn Thr Val Ile Asp Asn
6261 340 345 350
6263 Leu Ile Gly Phe Gln Glu Asn Asn Asp Ser Leu Leu Lys Ile Ile Asn
6264 355 360 365
6266 Gly Asn Asn Gln Pro Ile Leu Asp Thr Ser Ser Phe Lys Lys Gln Ile
6267 370 375 380
6269 Ser Gln Ile Asp Lys Lys Ile Gln Lys Asn Ser Asp Leu Tyr Leu Asn
6270 385 390 395 400
6272 Asp Phe Ile Thr Met Asp Glu Leu Lys Asp Arg Thr Asp Ser Leu Gln
6273 405 410 415
6275 Ala Glu Lys Lys Leu Leu Lys Ala Lys Ile Ser Glu Asn Lys Phe Asn
6276 420 425 430
6278 Asp Ser Thr Asp Val Phe Glu Leu Val Lys Thr Gln Leu Gly Ser Ile
6279 435 440 445
6281 Pro Ile Asn Glu Leu Ser Tyr Asp Asn Lys Lys Ile Val Asn Asn
6282 450 455 460
6284 Leu Val Ser Lys Val Asp Val Thr Ala Asp Asn Val Asp Ile Ile Phe
6285 465 470 475 480
6287 Lys Phe Gln Leu Ala

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PATENT APPLICATION: US/10/014,099A

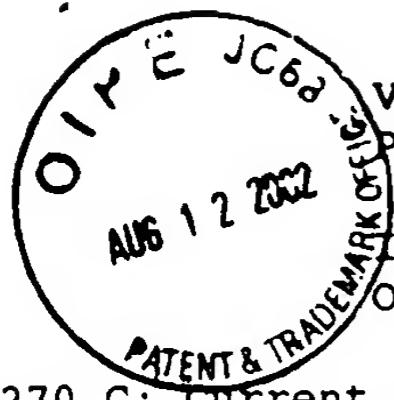
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6288
E--> 6294 1

485

Remove extra material at
end of file.



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L:15 M:270 C: Current Application Number differs, Replaced Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:262 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:263 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:921 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:922 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:928 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:480
L:1412 M:283 W: Missing Blank Line separator, <220> field identifier
L:1532 M:252 E: No. of Seq. differs, <211> LENGTH:Input:620 Found:0 SEQ:23
L:3325 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:65
L:3328 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:65
L:3533 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:67
L:3536 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:67
L:3736 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:69
L:3739 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:69
L:6294 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:108

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